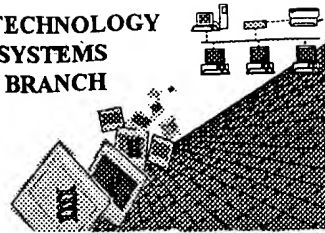


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/749,728A  
Source: OIP  
Date Processed by STIC: 2/8/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09-749,728A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 80 and more missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002

TIME: 11:44:39

Input Set : A:\766.43 Sequence Listing.txt  
 Output Set: N:\CRF3\02082002\I749728A.raw

*pp 1-4*  
 Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: Umezawa, Akihiro  
 4 Hata, Jun-Ichi  
 5 Fukuda, Keiichi  
 6 Ogawa, Satoshi  
 7 Sakurada, Kazuhiro  
 8 Gojo, Satoshi  
 9 Yamada, Yoji  
 11 <120> TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO  
 CARDIOMYOCYTES  
 13 <130> FILE REFERENCE: 00766.000043  
 15 <140> CURRENT APPLICATION NUMBER: US/09/749,728A  
 16 <141> CURRENT FILING DATE: 2001-09-17  
 18 <150> PRIOR APPLICATION NUMBER: H11-372826  
 19 <151> PRIOR FILING DATE: 1999-12-28  
 21 <150> PRIOR APPLICATION NUMBER: PCT-JP00-01148  
 22 <151> PRIOR FILING DATE: 2000-02-28  
 24 <150> PRIOR APPLICATION NUMBER: PCT-JP00-07741  
 25 <151> PRIOR FILING DATE: 2000-11-02  
 27 <160> NUMBER OF SEQ ID NOS: 80  
 29 <170> SOFTWARE: PatentIn Ver.2.0

## ERRORED SEQUENCES

343 <210> SEQ ID NO: 7  
 344 <211> LENGTH: 155  
 345 <212> TYPE: PRT  
 346 <213> ORGANISM: Homo sapiens  
 347 <400> SEQUENCE: 7  
 348 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly  
 349 1 5 10 15  
 350 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu  
 351 20 25 30  
 352 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg  
 353 35 40 45  
 354 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu  
 355 50 55 60  
 356 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn  
 357 65 70 75 80  
 358 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys  
 359 85 90 95  
 360 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr  
 361 100 105 110  
 362 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002  
 TIME: 11:44:39

Input Set : A:\766.43 Sequence Listing.txt  
 Output Set: N:\CRF3\02082002\I749728A.raw

363 115 120 125  
 364 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys  
 365 130 135 140  
 366 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser  
 E--> 367 145 150 *1556 insert*  
 850 <210> SEQ ID NO: 15  
 851 <211> LENGTH: 365  
 852 <212> TYPE: PRT  
 853 <213> ORGANISM: Homo sapiens  
*OK* 854 <400> SEQUENCE: 15  
 855 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn  
 856 1 5 10 15  
 857 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala  
 858 20 25 30  
 859 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe  
 860 35 40 45  
 861 Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg  
 862 50 55 60  
 863 Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr  
 864 65 70 75 80  
 865 Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp  
 866 85 90 95  
 867 Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys  
 868 100 105 110  
 869 Phe Arg Arg Leu Ala Gly Glu Gly Asp Pro Ala Leu Pro Arg Pro  
 870 115 120 125  
 871 Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr  
 872 130 135 140  
 873 Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala  
 874 145 150 155 160  
 875 Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys  
 876 165 170 175  
 877 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu  
 878 180 185 190  
 879 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg  
 880 195 200 205  
 881 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr  
 882 210 215 220  
 883 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr  
 884 225 230 235 240  
 885 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro  
 886 245 250 255  
 887 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro  
 888 260 265 270  
 889 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg  
 890 275 280 285  
 891 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys  
 892 290 295 300  
 893 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys

## RAW SEQUENCE LISTING

DATE: 02/08/2002

PATENT APPLICATION: US/09/749,728A

TIME: 11:44:40

Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\02082002\I749728A.raw

```

894 305          310          315          320
895 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
896          325          330          335
897 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
898          340          345          350
899 Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
E--> 900          355          360          365<
1401 <210> SEQ ID NO: 23
1402 <211> LENGTH: 215
1403 <212> TYPE: PRT
1404 <213> ORGANISM: Homo sapiens
OK-> 1405 <400> SEQUENCE: 23
1406 Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro
1407 1          5          10          15
1408 His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
1409          20          25          30
1410 Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
1411          35          40          45
1412 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
1413          50          55          60
1414 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
1415 65          70          75          80
1416 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
1417          85          90          95
1418 Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
1419          100          105          110
1420 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
1421          115          120          125
1422 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
1423          130          135          140
1424 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
1425 145          150          155          160
1426 Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
1427          165          170          175
1428 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
1429          180          185          190
1430 Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
1431          195          200          205
1432 Trp Ala Leu Glu Leu Asn Gln
E--> 1433          210          215<
2651 <210> SEQ ID NO: 63
2652 <211> LENGTH: 215
2653 <212> TYPE: PRT
2654 <213> ORGANISM: Homo sapiens
OK-> 2655 <400> SEQUENCE: 63
2656 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
2657 1          5          10          15
2659 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
2660          20          25          30

```

## RAW SEQUENCE LISTING

DATE: 02/08/2002

PATENT APPLICATION: US/09/749,728A

TIME: 11:44:40

Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\02082002\I749728A.raw

```

2662 Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
2663          35                      40                      45
2665 Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
2666          50                      55                      60
2668 Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
2669 65          70                      75                      80
2671 Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
2672          85                      90                      95
2674 Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
2675          100                     105                     110
2677 Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
2678          115                     120                     125
2680 Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
2681          130                     135                     140
2683 Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
2684 145          150                     155                     160
2686 Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
2687          165                     170                     175
2689 Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
2690          180                     185                     190
2692 Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
2693          195                     200                     205
2695 Thr Trp Ala Pro Glu Pro Arg
2696          210

```

E--&gt;

3200 &lt;210&gt; SEQ ID NO: 80

3201 &lt;211&gt; LENGTH: 19

3202 &lt;212&gt; TYPE: DNA

3203 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 3204 &lt;220&gt; FEATURE:

W--&gt; 3204 &lt;223&gt; OTHER INFORMATION:

W--&gt; 3204 &lt;400&gt; SEQUENCE: 80

3205 ggggtgctcag gtagtggtt

E--&gt; 3208 my\_main 231957v1 delete

see item 11 on Error Summary sheet

The types of errors shown exist throughout the Sequence Listing. Please check sequences for similar errors. all

## VERIFICATION SUMMARY

DATE: 02/08/2002

PATENT APPLICATION: US/09/749,728A

TIME: 11:44:41

Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\02082002\I749728A.raw

L:35 M:283 W: Missing Blank Line separator, <400> field identifier  
L:92 M:283 W: Missing Blank Line separator, <220> field identifier  
L:95 M:283 W: Missing Blank Line separator, <400> field identifier  
L:178 M:283 W: Missing Blank Line separator, <400> field identifier  
L:209 M:283 W: Missing Blank Line separator, <220> field identifier  
L:212 M:283 W: Missing Blank Line separator, <400> field identifier  
L:256 M:283 W: Missing Blank Line separator, <400> field identifier  
L:292 M:283 W: Missing Blank Line separator, <220> field identifier  
L:295 M:283 W: Missing Blank Line separator, <400> field identifier  
L:347 M:283 W: Missing Blank Line separator, <400> field identifier  
L:367 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:372 M:283 W: Missing Blank Line separator, <220> field identifier  
L:375 M:283 W: Missing Blank Line separator, <400> field identifier  
L:410 M:283 W: Missing Blank Line separator, <400> field identifier  
L:457 M:283 W: Missing Blank Line separator, <220> field identifier  
L:460 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:283 W: Missing Blank Line separator, <400> field identifier  
L:589 M:283 W: Missing Blank Line separator, <220> field identifier  
L:592 M:283 W: Missing Blank Line separator, <400> field identifier  
L:681 M:283 W: Missing Blank Line separator, <400> field identifier  
L:750 M:283 W: Missing Blank Line separator, <220> field identifier  
L:753 M:283 W: Missing Blank Line separator, <400> field identifier  
L:854 M:283 W: Missing Blank Line separator, <400> field identifier  
L:900 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15  
L:905 M:283 W: Missing Blank Line separator, <220> field identifier  
L:908 M:283 W: Missing Blank Line separator, <400> field identifier  
L:982 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1046 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1049 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1144 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1215 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1218 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1322 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1355 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1358 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1405 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1433 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23  
L:1438 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1441 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1488 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1545 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1548 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1631 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1690 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1693 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1779 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1839 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1842 M:283 W: Missing Blank Line separator, <400> field identifier

## VERIFICATION SUMMARY

DATE: 02/08/2002

PATENT APPLICATION: US/09/749,728A

TIME: 11:44:41

Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\02082002\I749728A.raw

L:1931 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2078 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2081 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2299 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2301 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2696 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:63  
L:3141 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3141 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3148 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3148 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3155 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3155 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3162 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3162 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3169 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3169 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3176 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3176 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3183 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3183 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3190 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3190 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3197 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3197 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3204 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3204 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3208 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:80  
L:3208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:80  
L:3208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:3208 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:27 SEQ:80  
L:3208 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:3208 M:112 C: (48) String data converted to lower case,  
L:3208 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:27 SEQ:80